

**AMENDMENTS TO THE SPECIFICATION**

Insert the attached sheet entitled "Abstract" after the claims as page number 50.

Insert the Sequence Listing as separately numbered pages 1 - 86 after the abstract.

Replace the paragraph beginning at page 6, line 4 with the following amended paragraph:

**Figure 3. (a) ~~The~~ The** amino acid sequence of IL-6R extracellular domain (**SEQ ID No: 83**), showing the CBD comprising domain D2 (residues 92 to 195) and domain D3 (residues 196 to 297). The position of  $\beta$ -sheet structures are indicated by #. The position of loops in the cytokine binding region are shown by \* and marked L1 to L7. The Pro94, Pro95, Cys102, Cys103, Trp115, Cys146, Cys157, Pro199, Pro200, Trp219, Arg274, Trp284, Ser285, Trp287 and Ser288 residues are all conserved in known CBDs. The Leu100, Leu108, Val111, Ala127, Leu129, Val131, Leu159, Tyr169, Val171, Met173, Val175, Phe189, Gly191, Ile194, Leu195, Pro197, Ile203, Val205, Leu215, Val217, Leu232, Phe234, Leu236, Tyr238, Phe246, Trp249, Ile260, Ala263, Val271, Leu273, and Glu286 residues are mainly conserved hydrophobic residues in known CBDs. The Pro98, Pro117, Trp225, Cys258, His269, Ala291 and Gly293 are, in the majority, conserved residues in all known CBDs.

Replace the paragraph beginning at page 6, line 16 with the following amended paragraph:

**~~Figure 3(b)~~ Figure 3A** depicts the sequence alignment of the CBDs from IL-6R, IL-11R, PRLR and GCSR. Loops L1 to L7 are outlined by boxes.

Replace the paragraph beginning at page 6, line 23 with the following amended paragraph:

**Figure 5.** Comparison of the sequences of CBDs from a number of known ~~77~~  
~~known~~ genes (SEQ ID Nos:1-82). Figure 5A compares the sequences in the "first" FnIII  
domain, containing loops 1 to 4, and Figure 5B the sequences in the "second" FnIII  
domain, containing the loops 5-7. Conserved residues as described in Example 3 for the  
IL-6 receptor are aligned according to their sequence homologies. For example the  
hydrophobic residues, the cysteine residues (C) and in some cases two prolines side by  
side (PP) are aligned. The location of the 7 binding loops is indicated by the double-  
headed arrows..

Replace the paragraph beginning at page 35, line 16 with the following amended paragraph:

The partial DNA sequence of IL-6R D3 (loops 6 and 7 in bold and boxed, and  
Cys258 in bold) is shown below as sequence (a). The corresponding partial DNA  
sequence of the D3 library clone, showing changes in loop 6 and at Cys258 (mutated to  
Ser) shown as sequence (b).

(a) R S K T F T T W **M V K D L** Q H H C V I H D A W S G L R H  
(b) R S K T F T T W **A Q S R W** Q H H S V I H D A W S G L R H

(a) V V Q L R A **Q E E F G Q G** E W S E W (SEQ ID No:84)  
(b) V V Q L R A **Q E E F G Q G** E W S E W (SEQ ID No:85)

Replace the paragraph beginning at page 35, line 32 (and ending at page 36, line 2) with the  
following amended paragraph:

The partial DNA sequence of IL-6R D3 (loops 6 and 7 in bold and boxed, and  
Cys258 in bold) is shown below as sequence (c). The corresponding partial DNA

sequence of the D3 library clone, showing changes in loops 6 and 7 and at Cys258  
(mutated to Ser) shown as sequence (d).

(c) R S K T F T T W **M V K D L** Q H H C V I H D A W S G L R H  
(d) R S K T F T T W **S R Q N D** Q H H S V I H D A W S G L R H

(c) V V Q L R A **Q E E F G Q G** E W S E W (SEQ ID No:86)  
(d) V V Q L R A **R N E V R V G** E W S E W (SEQ ID No:87)

Replace the paragraph beginning at page 37, line 3 with the following amended paragraph:

The CBD of human prolactin receptor has the following amino acid sequence  
(SEQ ID No:21):

24 GQLPPGK PEIFKCR**SPN KETFT**CWWRP GTDGGGLPTNY  
L1  
61 SLT**YHREGET** L**MHECPDYIT** GGPNSCH**FGK QYTSMWR**TYI  
L2 L3  
101 MMVNATNQMG SSFSDE**LYVD** VT**YIVQPDPP** LELAVEVKQP  
L4  
141 EDRKPYLWIK WSPPTL**IDLK TGWFT**LLYEI RLKPEKAAEW  
L5  
181 EIHFA**GQQTE** F**KILSLHPGQ** KYLVQVR**CKP DHGY**WSAWSP  
L6 L7  
221 ATFIQIPSD 229

The first FnIII-like domain is defined by amino acids Glu24 to Val125 and the second  
Fn-III like domain by Gln126 to Asp229. Loops L1 to L7 are indicated as boxed residues  
on the above sequence.

Replace the paragraph beginning at page 38, line 3 with the following amended paragraph:

The CBD of IL-11R has the following amino acid sequence (SEQ ID No:27):

```
111  YPPARPVVSC QAADYENFSC TWSPSQISGL PTRYLTSYRK
                        L1
151  KTVLGADSQR RSPSTGPWPC PQDPLGAARC VVHGAEFWSQ
                        L2                                L3
191  YRINVTEVNP LGASTRLLDV SLQSIILRPDP PQGLRVESVP
                        L4
231  GYPRRLRASW TYPASWPCQP HFLKFKRLQY RPAQHPAWST
                        L5
271  VEPAGLEEV I TDAVAGLPHA VRVSARDFLD AGTWSTWSPE
                        L6                                L7
321  AWGTPSTGT 329
321  AWGTPSTG 328
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The first FnIII-like domain is defined by amino acids 112-214 and the second FnIII-like domain by amino acids 218-318. Loops L1 to L7 are indicated as boxed residues on the above sequence.

Replace the paragraph beginning at page 38, line 31 with the following amended paragraph:

The first FnIII-like domain derived from the CBD of prolactin receptor is defined by residues 24-125 ~~[IS THIS CORRECT—see Ex 9 questions]~~ as in Example 9.

Replace the paragraph beginning at page 38, line 34 (and ending on page 39, line 8) with the following amended paragraph:

The CBD of GSCFR has the following amino acid sequence (SEQ ID No:2):

```
121  YPPAIPHNLS  CLMNLTTSSL ICQWEPGPET HLPTSFTLKS
                        L1
161  FKSRGNCQTQ GDSILDCVPK DGQSHCCIPR KHLLLYQNMG
                        L2                        L3
201  IWVQAENALG TSMSPQLCLD PMDVVKLEPP MLRTMDPSPE
                        L4
241  AAPPQAGCLQ LCWEPWQPGL HINQKCELRH KPQRGEASWA
                        L5
281  LVGPLPLEAL QYELCGLLPA TAYTLQIRC RWPLPGHWSD
                        L6                        L7
321  WSPSLELRTT ERA  333
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Loops L1 to L7 of the CBD of GCSFR are indicated as boxed residues on the above sequence. The second region of the CBD of GCSFR is defined by residues 237-330.